

INPUT SET: S6937.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Adams, Craig W.
6 Pang, Patty P.-Y.
7 Belei, Marina8
9 (ii) TITLE OF INVENTION: Recombinant DNase B Derived from
10 Streptococcus pyogenes11
12 (iii) NUMBER OF SEQUENCES: 1613
14 (iv) CORRESPONDENCE ADDRESS:15 (A) ADDRESSEE: Sheldon & Mak
16 (B) STREET: 225 South Lake Avenue, Ninth Floor
17 (C) CITY: Pasadena
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 9100121
22 (v) COMPUTER READABLE FORM:23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.2527
28 (vi) CURRENT APPLICATION DATA:29 (A) APPLICATION NUMBER: US 08/482,785
30 (B) FILING DATE: 07-JUN-1995
31 (C) CLASSIFICATION: 43532
33 (vii) PRIOR APPLICATION DATA:34 (A) APPLICATION NUMBER: US/08/393,889
35 (B) FILING DATE: 24-FEB-199536
37 (A) APPLICATION NUMBER: US/08/082,845
38 (B) FILING DATE:39
40 (viii) ATTORNEY/AGENT INFORMATION:41 (A) NAME: Farber, Michael B.
42 (B) REGISTRATION NUMBER: 32,612
43 (C) REFERENCE/DOCKET NUMBER: 952144
45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (818) 796-4000

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47 (B) TELEFAX: (818) 795-6321
4849
50 (2) INFORMATION FOR SEQ ID NO:1:
5152 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 43 amino acids
54 (B) TYPE: amino acid
55 (D) TOPOLOGY: linear
5657 (ii) MOLECULE TYPE: peptide
5859 (iii) HYPOTHETICAL: NO
6061 (v) FRAGMENT TYPE: N-terminal
6263 (vi) ORIGINAL SOURCE:
64 (A) ORGANISM: Streptococcus pyogenes
6566 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
6768 Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys Arg Leu
69 1 5 10 15
7071
72 Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala Val Thr
73 20 25 30
7475
76 Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg
77 35 40
7879 (2) INFORMATION FOR SEQ ID NO:2:
8081 (i) SEQUENCE CHARACTERISTICS:
82 (A) LENGTH: 41 base pairs
83 (B) TYPE: nucleic acid
84 (C) STRANDEDNESS: single
85 (D) TOPOLOGY: linear
8687 (ii) MOLECULE TYPE: DNA (genomic)
8889 (iii) HYPOTHETICAL: NO
9091 (iv) ANTI-SENSE: NO
9293 (vi) ORIGINAL SOURCE:
94 (A) ORGANISM: Synthetic DNA primer
9596 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
9798
99

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41

100 TAACGGATCC GAATCTACTT GGATCAAGAC GGGTTTTTC T

101

102 (2) INFORMATION FOR SEQ ID NO:3:

103

104 (i) SEQUENCE CHARACTERISTICS:

105 (A) LENGTH: 41 base pairs
106 (B) TYPE: nucleic acid
107 (C) STRANDEDNESS: single
108 (D) TOPOLOGY: linear

109

110 (ii) MOLECULE TYPE: DNA (genomic)

111

112 (iii) HYPOTHETICAL: NO

113

114 (iv) ANTI-SENSE: NO

115

116 (vi) ORIGINAL SOURCE:

117 (A) ORGANISM: Synthetic DNA primer

118

119

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

121

122 CCGGGTCGAC CCGGGGAATG ACGGCAATCA TTGCTTTTC T

41

123

124 (2) INFORMATION FOR SEQ ID NO:4:

125

126 (i) SEQUENCE CHARACTERISTICS:

127 (A) LENGTH: 23 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear

130

131 (ii) MOLECULE TYPE: peptide

132

133 (iii) HYPOTHETICAL: NO

134

135 (v) FRAGMENT TYPE: N-terminal

136

137 (vi) ORIGINAL SOURCE:

138 (A) ORGANISM: Streptococcus pyogenes

139

140

141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

142

143 Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Xaa
144 1 5 10 15

145

146

147 Tyr Leu Asn Glu Ala Leu Ala

148 20

149

150 (2) INFORMATION FOR SEQ ID NO:5:

151

152 (i) SEQUENCE CHARACTERISTICS:

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153 (A) LENGTH: 22 base pairs
154 (B) TYPE: nucleic acid
155 (C) STRANDEDNESS: single
156 (D) TOPOLOGY: linear
157
158 (ii) MOLECULE TYPE: DNA (genomic)
159
160 (iii) HYPOTHETICAL: NO
161
162 (iv) ANTI-SENSE: NO
163
164 (vi) ORIGINAL SOURCE:
165 (A) ORGANISM: Synthetic probe
166
167
168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
169
170 CAUACNCART NWSNAAYGAY GT 22
171
172
173 (2) INFORMATION FOR SEQ ID NO:6:
174
175 (i) SEQUENCE CHARACTERISTICS:
176 (A) LENGTH: 38 amino acids
177 (B) TYPE: amino acid
178 (D) TOPOLOGY: linear
179
180 (ii) MOLECULE TYPE: peptide
181
182 (iii) HYPOTHETICAL: NO
183
184 (v) FRAGMENT TYPE: N-terminal
185
186 (vi) ORIGINAL SOURCE:
187 (A) ORGANISM: Streptococcus pyogenes
188
189
190
191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
192
193 Arg Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser
194 1 5 10 15
195
196
197 Lys Tyr Leu Asn Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn
198 20 25 30
199
200
201 Tyr Tyr Lys Thr Leu Gly
202 35
203
204 (2) INFORMATION FOR SEQ ID NO:7:
205

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206 (i) SEQUENCE CHARACTERISTICS:
207 (A) LENGTH: 1083 base pairs
208 (B) TYPE: nucleic acid
209 (C) STRANDEDNESS: double
210 (D) TOPOLOGY: linear
211
212 (ii) MOLECULE TYPE: DNA (genomic)
213
214 (iii) HYPOTHETICAL: NO
215
216 (iv) ANTI-SENSE: NO
217
218 (vi) ORIGINAL SOURCE:
219 (A) ORGANISM: *Streptococcus pyogenes*
220
221 (ix) FEATURE:
222 (A) NAME/KEY: CDS
223 (B) LOCATION: 129..944
224
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
227
228 GACAACGCCT TCTTTTTCT CCTTACTATC TCCTTTAATT TTCATATTTC TTAAAAAAAC 60
229
230 TATTGATAAA CTAGTTAAGT AAGCGTATAC TATGGTTAGT TAGCGAAATT AGAAAAGAGG 120
231
232 ACAAGCAT ATG AAT CTA CTT GGA TCA AGA CGG GTT TTT TCT AAA AAA TGT 170
233 Met Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys
234 1 5 10
235
236 CGG CTA GTA AAA TTT TCA ATG GTA GCT CTT GTA TCA GCC ACA ATG GCT 218
237 Arg Leu Val Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala
238 15 20 25 30
239
240 GTA ACA ACA GTC ACA CTT GAA AAT ACT GCA CTG GCA CGA CAA ACA CAG 266
241 Val Thr Thr Val Thr Leu Glu Asn Thr Ala Leu Ala Arg Gln Thr Gln
242 35 40 45
243
244 GTC TCA AAT GAT GTT CTA AAT GAT GGC GCA AGC AAG TAC CTA AAC 314
245 Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Lys Tyr Leu Asn
246 50 55 60
247
248 GAA GCA TTA GCT TGG ACA TTC AAT GAC AGT CCT AAC TAT TAC AAA ACT 362
249 Glu Ala Leu Ala Trp Thr Phe Asn Asp Ser Pro Asn Tyr Tyr Lys Thr
250 65 70 75
251
252 TTA GGT ACT AGT CAG ATT ACT CCA GCA CTC TTT CCT AAA GCA GGA GAT 410
253 Leu Gly Thr Ser Gln Ile Thr Pro Ala Leu Phe Pro Lys Ala Gly Asp
254 80 85 90
255
256 ATT CTC TAT AGC AAA TTA GAT GAG TTA GGA AGG ACG CGT ACT GCT AGA 458
257 Ile Leu Tyr Ser Lys Leu Asp Glu Leu Gly Arg Thr Arg Thr Ala Arg
258 95 100 105 110

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SEQUENCE VERIFICATION REPORT
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